

C1
9/2/12
(1) GENERAL INFORMATION:

- (i) APPLICANT: He, Wei-Wu et al.
- (ii) TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Ave.
(C) CITY: Rockville
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,969
(B) FILING DATE: 05-JUN-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/334,251
(B) FILING DATE: 11-NOV-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Brookes, A. Anders
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF140P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 301-309-8504
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGAAA CTTTGCTGTG CGCGTTCCTCC CGCGCGCGGG CTCAACTTTG TAGAGCGAGG

60

GGCCAACTTG GCAGAGCGCG CGGCCAGCTT TGCAGAGAGC GCCCTCCAGG GACTATGCGT	120
GCGGGGACAC GGGTCGCTTT GGGCTCTTCC ACCCTGCGG AGCGCACTAC CCCGAGCCAG	180
GGGCGGTGCA AGCCCCGCCC GGCCCTACCC AGGGCGGCTC CTCCCTCCGC AGCGCCGAGA	240
CTTTTAGTTT CGCTTTCGCT AAAGGGGCCC CAGACCCTTG CTGCGGAGCG ACGGAGAGAG	300
ACTGTGCCAG TCCCAGCCGC CCTACCGCCG TGGGAACGAT GGCAGATGAT TCAGGGCTGT	360
ATTGAAGAGC AGGGGGTTGA GGATTCAGCA AATGAAGATT CAGTGGATGC TAAGCCAGAC	420
CGGTCCTCGT TTGTACCGTC CCTCTTCAGT AAGAAGAAGA AAAATGTCAC CATGCGATCC	480
ATCAAGACCA CCCGGGACCG AGTGCCTACA TATCAGTACA ACATGAATTT TGAAAAGCTG	540
GGCAAATGCA TCATAATAAA CAACAAGAAC TTTGATAAAG TGACAGGTAT GGGCGTTCTGA	600
AACGGAACAG ACAAAGATGC CGAGGCGCTC TTCAAGTGCT TCCGAAGCCT GGGTTTTGAC	660
GTGATTGTCT ATAATGACTG CTCTTGTGCC AAGATGCAAG ATCTGCTTAA AAAAGCTTCT	720
GAAGAGGACC ATACAAATGC CGCCTGCTTC GCCTGCATCC TCTTAAGCCA TGGAGAAGAA	780
AATGTAATTT ATGGGAAAGA TGGTGTGACA CCAATAAAGG ATTTGACAGC CCACTTTAGG	840
GGGGATAGAT GCAAAACCCT TTTAGAGAAA CCAAACTCT TCTTCATTCA GGCTTGCCGA	900
GGGACCGAGC TTGATGATGG CATCCAGGCC GACTCGGGGC CCATCAATGA CACAGATGCT	960
AATCCTCGAT ACAAGATCCC AGTGGAAGCT GACTTCCTCT TCGCCTATTC CACGGTTCCA	1020
GGCTATTACT CGTGAGGAG CCCAGGAAGA GGCTCCTGGT TTGTGCAAGC CCTCTGCTCC	1080
ATCCTGGAGG AGCACGGAAA AGACCTGGAA ATCATGCAAA TCCTCCACCA GGGTGAATGA	1140
CAGAGTTGCC AGGCACTTTG AGTCTCAGTC TGATGACCCA CACTTCCATG AGAAGAAGCA	1200
GATCCCCGTG GTGGTCTCCA TGCTCACCAA GGAAGTCTAC TTCAGTCAAT AGCCATATCA	1260
GGGGTACATT CTAGCTGAGA AGCAATGGGT CACTCATTA TGAATCACAT TTTTTATGC	1320
TCTTGAAATA TTCAGAAATT CTCCAGGATT TTAATTCAG GAAAATGTAT T	1371

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser

1	5	10	15
Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val	20	25	30
Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile	35	40	45
Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe	50	55	60
Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys	65	70	75
Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala	85	90	95
Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn	100	105	110
Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu	115	120	125
Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His	130	135	140
Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys	145	150	155
Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu	165	170	175
Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp	180	185	190
Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn	195	200	205
Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser	210	215	220
Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp	225	230	235
Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Glu Leu	245	250	255
Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His	260	265	270
Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile	275	280	285
Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	290	295	300

(2) INFORMATION FOR SEQ-ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG ATGGGTGCTA TTGTGAGGCG GTTGTAGAAG AGTTTCGTGA GTGCTCGCAG	60
CTCATACCTG TGGCTGTGTA TCCGTGGCCA CAGCTGGTTG GCGTCGCCTT GAAATCCCAG	120
GCCGTGAGGA GTTAGCGAGC CCTGCTCACA CTCGGCGCTC TGGTTTTCGG TGGGTGTGCC	180
CTGCACCTGC CTCTCCCGC ATTCTCATTA ATAAAGGTAT CCATGGAGAA CACTGAAAAC	240
TCAGTGGATT CAAAATCCAT TAAAAATTTG GAACCAAGA TCATACATGG AAGCGAATCA	300
ATGGACTCTG GAATATCCCT GGACAACAGT TATAAATGG ATTATCCTGA GATGGGTTTA	360
TGTATAATAA TTAATAATAA GAATTTTCAT AAAAGCACTG GAATGACATC TCGGTCTGGT	420
ACAGATGTCG ATGCAGCAAA CCTCAGGGAA ACATTCAGAA ACTTGAAATA TGAAGTCAGG	480
AATAAAAATG ATCTTACACG TGAAGAAATT GTGGAATTGA TGCGTGATGT TTCTAAAGAA	540
GATCACAGCA AAAGGAGCAG TTTGTGTTGT GTGCTTCTGA GCCATGGTGA AGAAGGAATA	600
ATTTTTGGAA CAAATGGACC TGTGAGCTG AAAAAATAA CAAACTTTTT CAGAGGGGAT	660
CGTTGTAGAA GTCTAACTGG AAAACCCAAA CTTTTCATTA TTCAGGCCTG CCGTGGTACA	720
GAAGTGGACT GTGGCATTGA GACAGACAGT GGTGTTGATG ATGACATGGC GTGTCATAAA	780
ATACCAGTGG AGGCCGACTT CTTGTATGCA TACTCCACAG CACCTGGTTA TTATTCTTGG	840
CGAAATTCAA AGGATGGCTC GTGGTTCATC CAGTCGCTTT GTGCCATGCT GAAACAGTAT	900
GCCGACAAGC TTGAATTTAT GCACATTCTT ACCCGGGTTA ACCGAAAGGT GGCAACAGAA	960
TTGAGTCCT TTTCTTTTGA CGCTACTTTT CATGCAAAGA AACAGATTCC ATGTATTGTT	1020
TCCATGCTCA CAAAAGAACT CTATTTTTAT CACTAAAGAA ATGGTTGGTT GGTGGTTTTT	1080
TTAGTTTGT ATGCCAAGTG AGAAGATGGT ATATTGGGT ACTGTATTTC CCTCTCATTG	1140
GGGACCTACT CTCATGCTG	1159

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Asn	Thr	Glu	Asn	Ser	Val	Asp	Ser	Lys	Ser	Ile	Lys	Asn	Leu	1	5	10	15
Glu	Pro	Lys	Ile	Ile	His	Gly	Ser	Glu	Ser	Met	Asp	Ser	Gly	Ile	Ser	20	25	30	
Leu	Asp	Asn	Ser	Tyr	Lys	Met	Asp	Tyr	Pro	Glu	Met	Gly	Leu	Cys	Ile	35	40	45	
Ile	Ile	Asn	Asn	Lys	Asn	Phe	His	Lys	Ser	Thr	Gly	Met	Thr	Ser	Arg	50	55	60	
Ser	Gly	Thr	Asp	Val	Asp	Ala	Ala	Asn	Leu	Arg	Glu	Thr	Phe	Arg	Asn	65	70	75	80
Leu	Lys	Tyr	Glu	Val	Arg	Asn	Lys	Asn	Asp	Leu	Thr	Arg	Glu	Glu	Ile	85	90	95	
Val	Glu	Leu	Met	Arg	Asp	Val	Ser	Lys	Glu	Asp	His	Ser	Lys	Arg	Ser	100	105	110	
Ser	Phe	Val	Cys	Val	Leu	Leu	Ser	His	Gly	Glu	Glu	Gly	Ile	Ile	Phe	115	120	125	
Gly	Thr	Asn	Gly	Pro	Val	Asp	Leu	Lys	Lys	Ile	Thr	Asn	Phe	Phe	Arg	130	135	140	
Gly	Asp	Arg	Cys	Arg	Ser	Leu	Thr	Gly	Lys	Pro	Lys	Leu	Phe	Ile	Ile	145	150	155	160
Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Cys	Gly	Ile	Glu	Thr	Asp	Ser	165	170	175	
Gly	Val	Asp	Asp	Asp	Met	Ala	Cys	His	Lys	Ile	Pro	Val	Glu	Ala	Asp	180	185	190	
Phe	Leu	Tyr	Ala	Tyr	Ser	Thr	Ala	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Asn	195	200	205	
Ser	Lys	Asp	Gly	Ser	Trp	Phe	Ile	Gln	Ser	Leu	Cys	Ala	Met	Leu	Lys	210	215	220	
Gln	Tyr	Ala	Asp	Lys	Leu	Glu	Phe	Met	His	Ile	Leu	Thr	Arg	Val	Asn	225	230	235	240
Arg	Lys	Val	Ala	Thr	Glu	Phe	Glu	Ser	Phe	Ser	Phe	Asp	Ala	Thr	Phe	245	250	255	
His	Ala	Lys	Lys	Gln	Ile	Pro	Cys	Ile	Val	Ser	Met	Leu	Thr	Lys	Glu	260	265	270	
Leu	Tyr	Phe	Tyr	His												275			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC ATGCGTGCGG GGACACGGGT C

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTACTCTAGA TCATTCACCC TGGTGGAGGA T

31

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCGGATCC ATGGAGAACA CTGAAACTC A

31

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTACTCTAGA TTAGTGATAA AAATAGAGTT C

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTATGCGT GCGGGGACAC GG

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATCAAGCGT AGTCTGGGAC GTCGTATGGG TATTCACCCT GGTGGAGGAT TTG

53

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGGAGA ACACTGAAAA C

- 21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATCAAGCGT AGTCTGGGAC GTCGTATGGG TAGTGATAAA AATAGAGTTC TTT

53

CF
Conclude